

5' ... ATAGAATAC A GCATGTC TCC CGGCCG CCATGG CCCCGG GATTGGC ATG AGG CAA CCT AAC CCT TGC AGC . . .

S _{P6} Promoter<	SphI	EagI	NcoI	SacII	BspHI
---------------------------	-------------	-------------	-------------	--------------	--------------

ANG SEQUENCE . . . GTC CCC CAA CAA GCT TCA TGC ATA TGG AGT ATG GTC TAG GGATCC

HindIII	NdeI	BamHI
---------	------	-------

GGGTACCGAGCTCGAATTCGCCCTATA. . . 3'

KpnI SacI EcoRI |> T7 Promoter

Figure 1

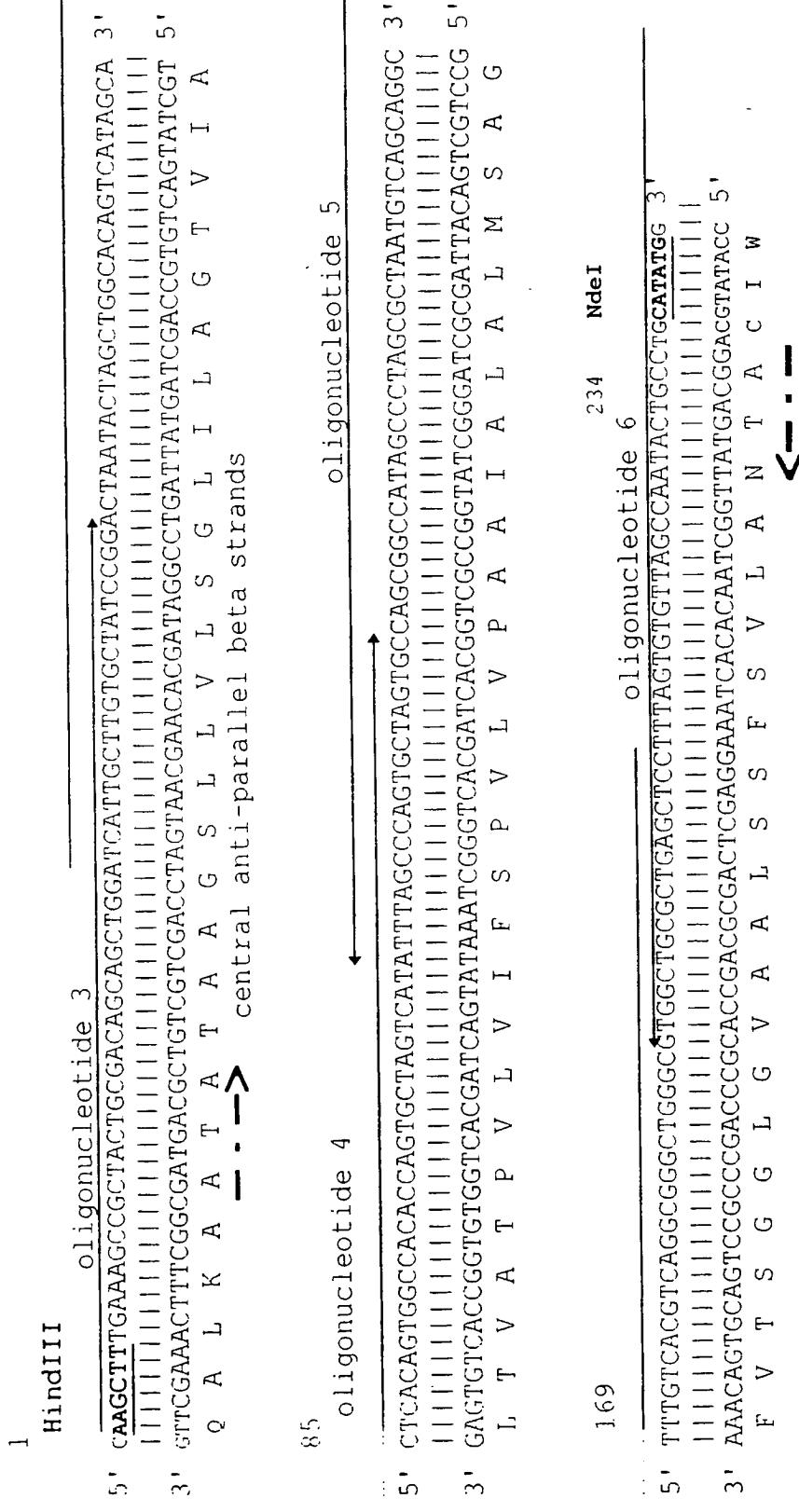


Figure 2

1
ATGAGGCAACTAAACCCTTGAGCCAAGAGTTGCAATCACCAACAATCATATCTGCCG
M R Q L N P Cys S Q E L Q S P Q Q S Y L Q

61
CAGCCATATCCACAAAACCCATATCTACCGCAAAAACCATTCCAGTGCAGCAACCGTTT
Q P Y P Q N P Y L P Q K P F P V Q Q P F

121
CACACACCCCCAACAAATATTCCTATCTACCAAGAGGAATTGTTCCCCAATATCAAATA
H T P Q Q Y F P Y L P E E L F P Q Y Q I

181
CCAACCCCCCTACAACCAACCAACCAACCATTCCCCAACAAACCACAACACCTCTTCCTCGG
P T P L Q P Q P F P Q Q P Q Q P L P R

241
CCCCAACAAACCATTCCCCTGGCAACCACAACCAACCATTCCCCAGCCCCAACGAACCAATT
P Q Q P F P W Q P Q Q P F P Q P Q E P I

301
CCCCAGCAACCACAACCAACCATTCCCACAGCAACCACAACCAACCATTCCCACAGCAACCA
P Q Q P Q Q P F P Q Q P Q Q P F P Q Q P

361
CAACAAATAATTTCCAGCAACCCCCAACAAATCATACCCGTGCAACCTAACAGCCATT
Q Q I I F Q Q P Q Q S Y P V Q P Q Q P F

421
CCTCAACAAACCTCAACCAGTCCCCAACAA GCT TCA TGCATATGGAGTATGGCTAG 477
P Q Q P Q P V P Q Q A S Cys I W S M V ***

Figure 3

HindIII 1 54
AAGCTTCTACCACTCCCACCGCCGTGGCTGTGACTTCGATCTGACAGCTACCACCACTAC
 A S T T P T A V A V T F D L T A T T T Y

GGCGAGAACATCTACCTGGTCGGATCGATCTCAGCTGGGTGACTGGGAAACCAGCGAC 114
 G E N I Y L V G S I S Q L G D W E T S D

GGCATAGCTCTGAGTGCTGACAAGTACACTTCCAGCGACCCGCTCTGGTATGTCAGTGTG 174
 G I A L S A D K Y T S S D P L W Y V T V

ACTCTGCCGGCTGGTGAGTCGTTGAGTACAAGTTATCCGCATTGAGAGCGATGACTCC 234
 T L P A G E S F E Y K F I R I E S D D S

GTGGAGTGGGAGAGTGATCCCAACCGAGAATACACCGTCCTCAGGCGTGCAGAACGTCG 294
 V E W E S D P N R E Y T V P Q A C G T S

321 **NdeI**
 ACCGCGACGGTGACTGACACCTGGCGGTGCATATGG
 T A T V T D T W R C I W

Figure 4

5 / 17

HindIII 57
AAGCTTTCGGCAATGAAGATTGCACCCATGGATGAGTACTCTGATCACTCCACTCCAAAGC
A I G N E D C T P W M S T L I T P L P S
CM17. T

117
TGCCGTGACTATGTGGAACAACAAGCATGTCGCATCGAAACGCCGGTGCCTGACCTC
C R D Y V E Q Q A C R I E T P G S P Y L
. N . . . E M . . . P . .

177
GCCAAGCAGCAGTGTGCTGGGGAGCTTGCAAACATTCCGCAGCAGTGCCGATGCCAGGCG
A K Q Q C C G E L A N I P Q Q C R C Q A
. . . E . . E Q

237
CTGCGCTACTTCATGGGCCGAAGTCTCGTCCGGATCAGAGC GCCCTCATGGAACCTCCC
L R Y F M G P K S R P D Q S G L M E L P
.

297
GGATGCCCTAGGGAGGTGCAGATGGACTTCGTGAGGATACTCGTCACGCCGGGTACTGC
G C P R E V Q M D F V R I L V T P G Y C
. N . . P

354
AACTTGACGACC GTT CAC AAC ACTCCGTACTGCCTCGTATGGAGGAGTCTCAGTGG
N L T T V H N T P Y C L A M E E S Q W
.

357 **NdeI**
AGCTGCATATGG
S C I W

Figure 5

HindIII 57
AAGCTTACGATGTTGCTGGCGGGGTGGTGCTAACAAATGCCCTGTAGAGACAAAGCTAAAT
A Y D V A G G G G A Q Q C P V E T K L N

117
TCATGCAGGAATTACCTGCTAGATCGATGCTAACGATGAAGGATTCCCGGTACACCTGG
S C R N Y L L D R C S T M K D F P V T W

177
CGTTGGTGGAAATGGTGGAAAGGGAGGGTTGTCAAGAGCTCCTGGGAGTGTTGCAGTCGG
R W W K W W K G G C Q E L L G E C C S R

237
CTCGGCCAAATGCCACCGCAATGCCGCTGCAACATCATCCAGGGTCAATCCAAGGCGAT
L G Q M P P Q C R C N I I Q G S I Q G D

297
CTCGGTGGCATCTCGGATTCAGCGTGATCGGCAAGCAAAGTGATAACAAGAACGCAAG
L G G I F G F Q R D R A S K V I Q E A K

300
AACCTGCCGCCAGGTGCAACCAGGGCCCTCCCTGCAACATCCCCGGCACTATTGGCTAT
N L P P R C N Q G P P C N I P G T I G Y

363 **NdeI**
TACTGGTGCATATGG
Y W C I W

Figure 6

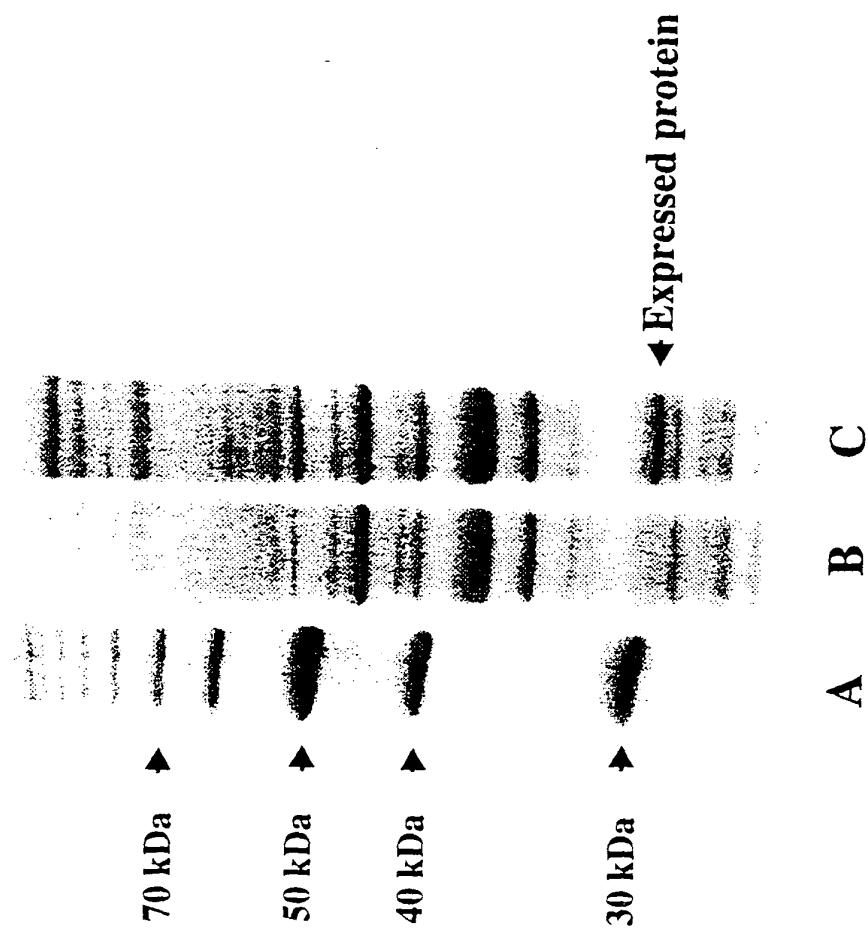


Figure 7

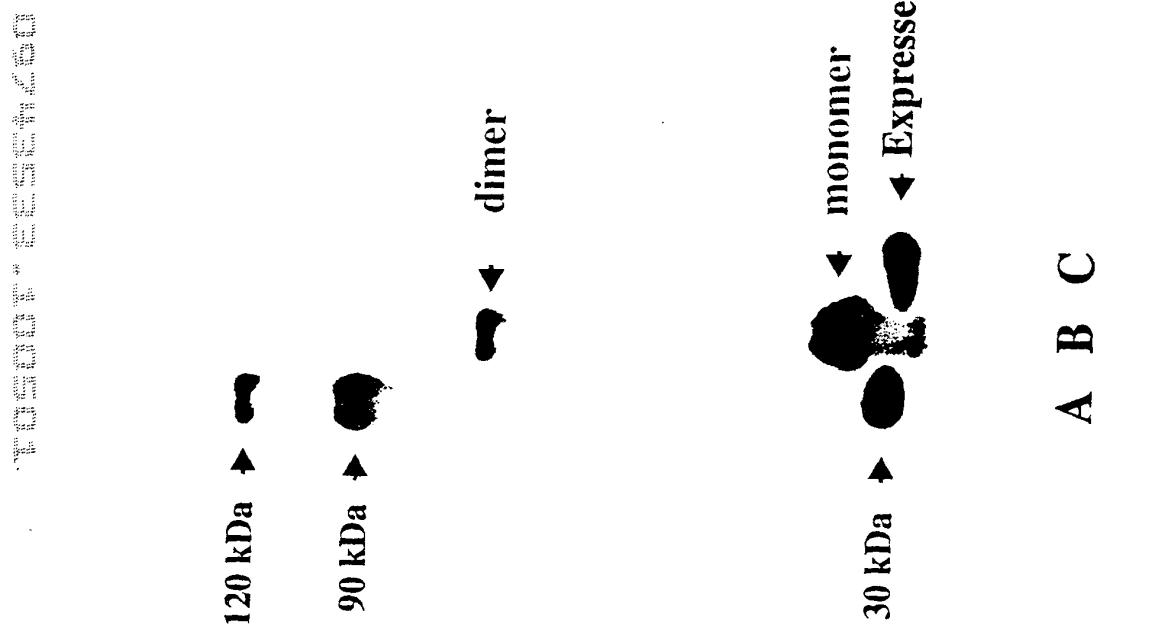


Figure 8

09 / 743533

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9 / 17

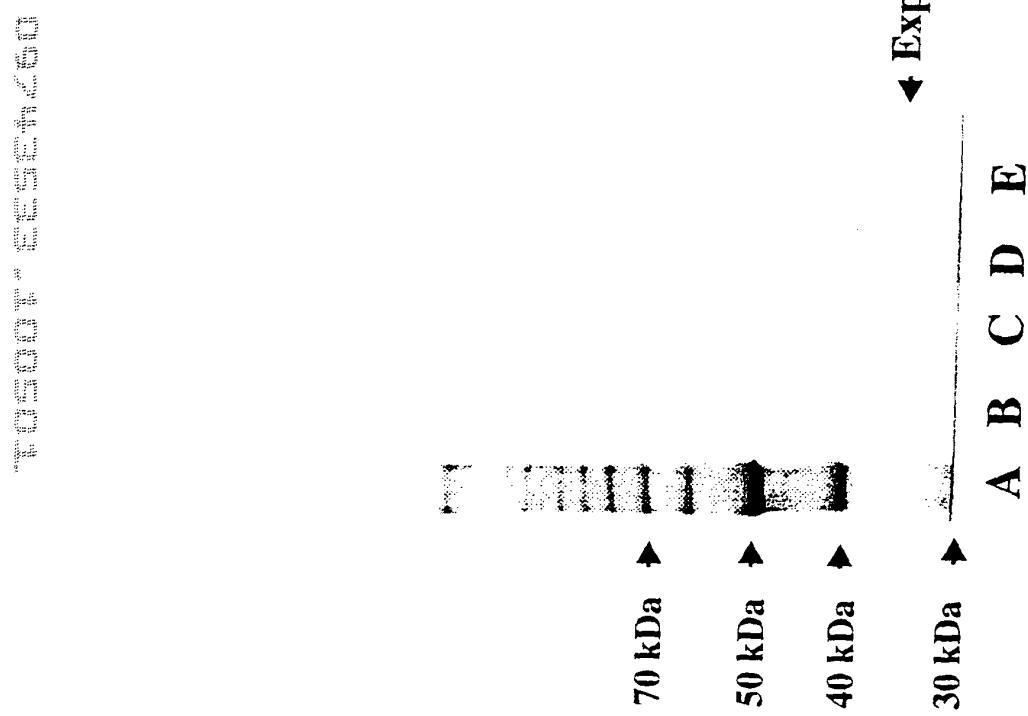


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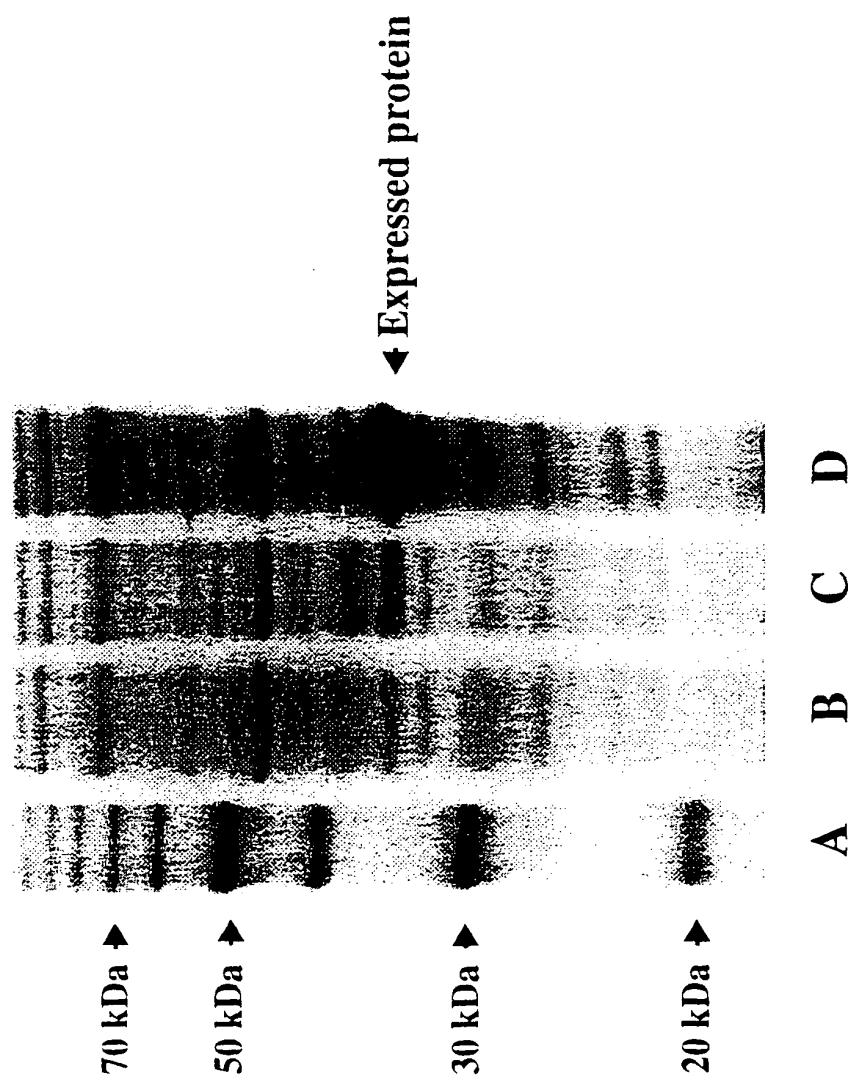


Figure 10

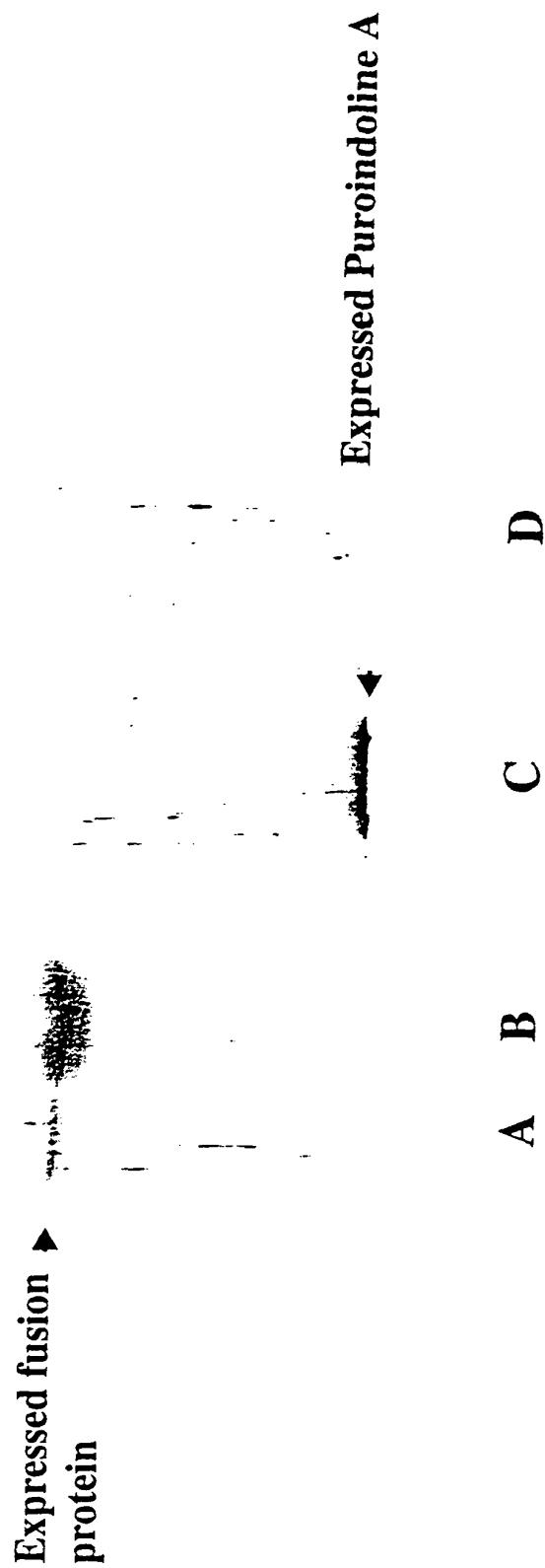


Figure 11

09/743533

PCT/AU99/00563

WO 00/02914

12 / 17

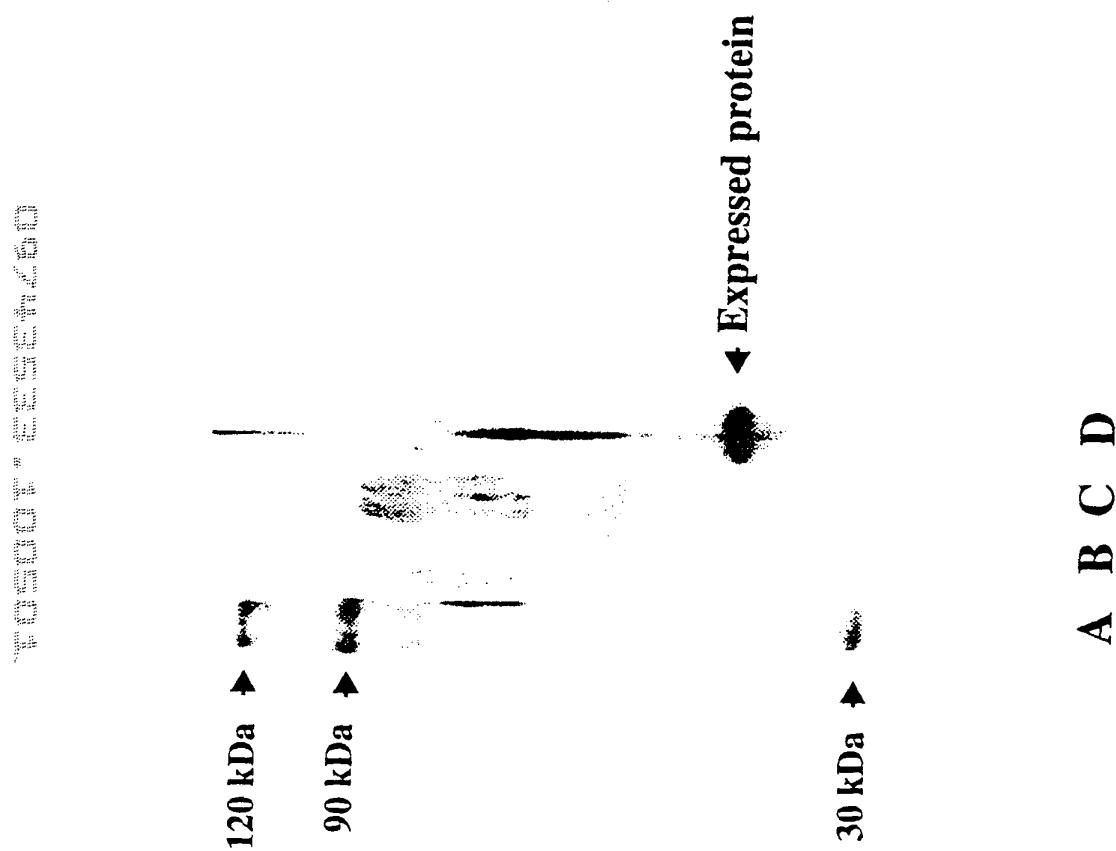


Figure 12

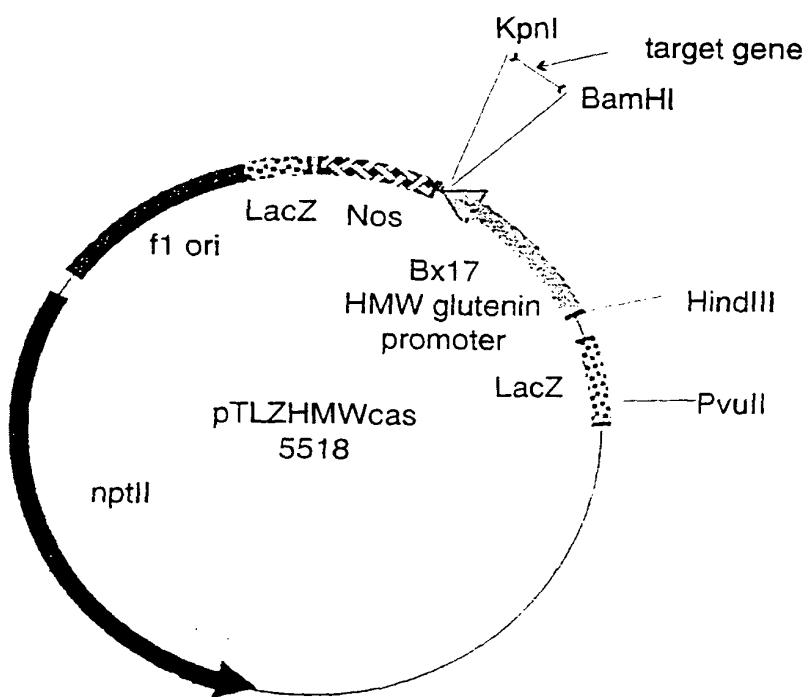


Figure 13

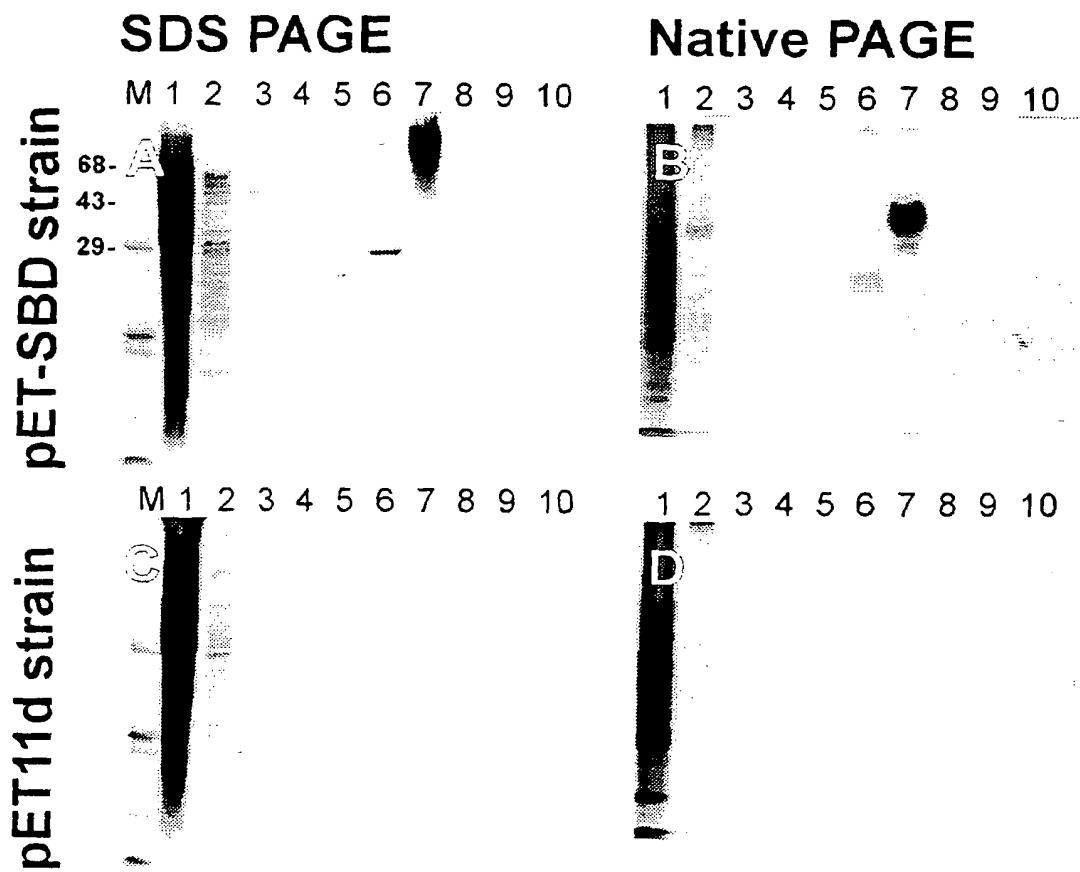


Figure 14

ANGCys7Cys236

binding domain in another protein

**ANG/insert/Cys7Cys236**

Figure 15

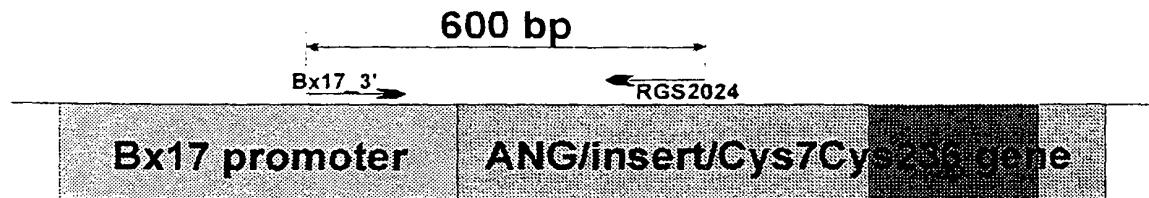


Figure 16

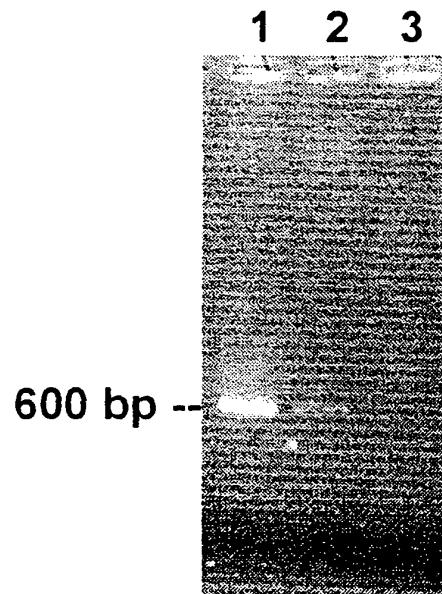


Figure 17

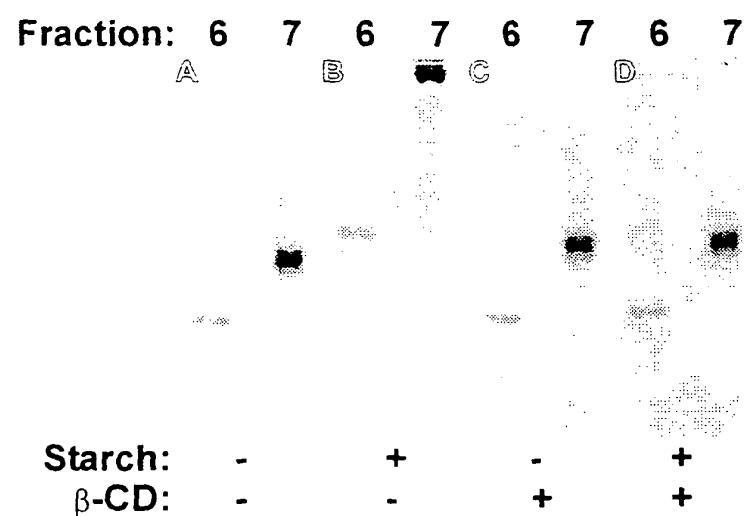


Figure 18

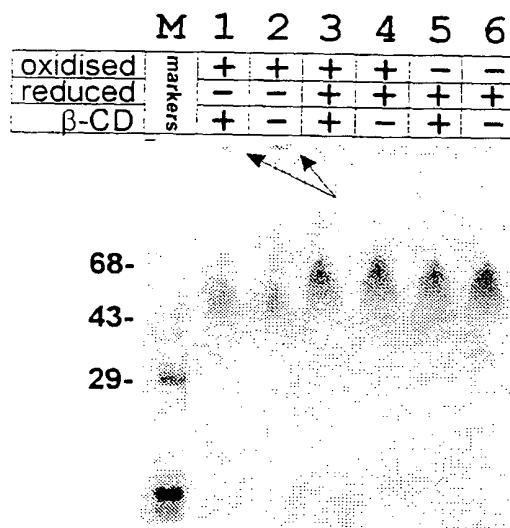


Figure 19